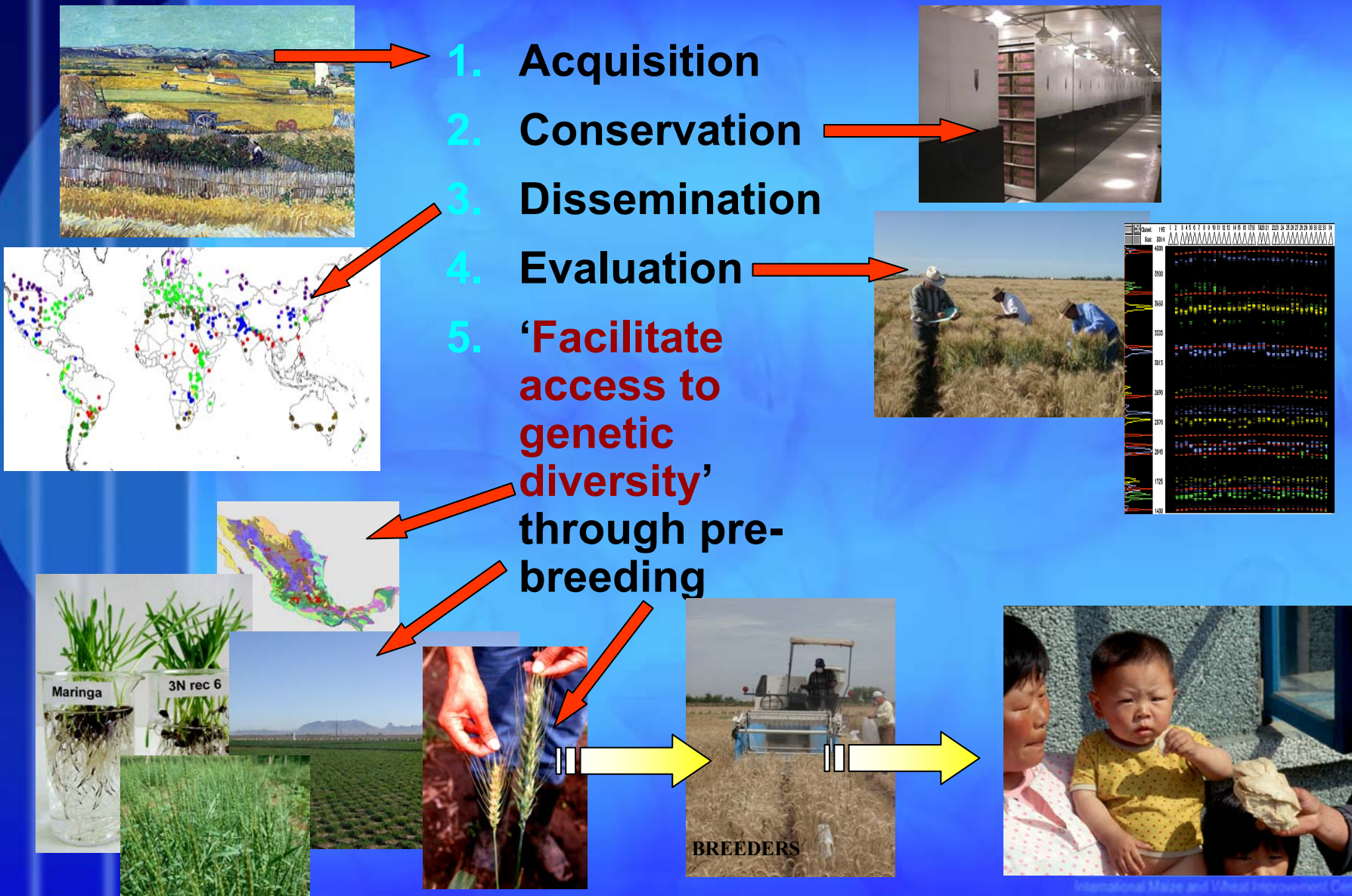


# CIMMYT GENETIC RESOURCES

- ◆ **Maarten van Ginkel**  
**Genetic Resources**  
**Program**  
**Head, CIMMYT Wheat**  
**Genebank and Related**  
**Pre-Breeding**  
**CIMMYT, Mexico**



# 'Output' from Genetic Resources



# Accessions

- ◆ **Total number of accessions: about 150,000 (duplications in process of being removed)**
  - **52% from CIMMYT breeders**
  - **42% landraces**
  - **6% wild relatives, species and others**
- ◆ **Too much of a good thing?**
- ◆ **Use GIS to pinpoint areas of origin and potential interest.**

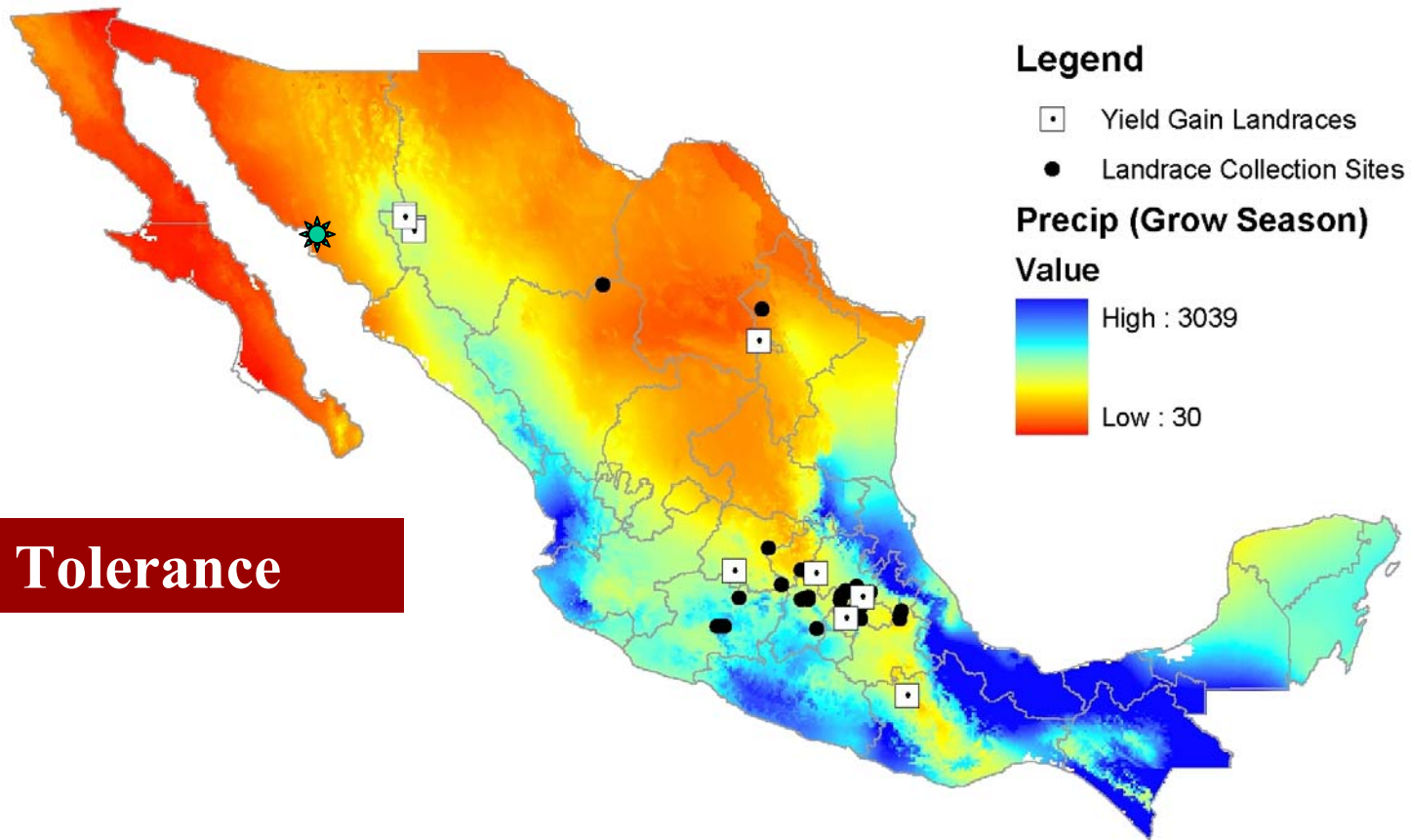


# **10,000 Mexican Wheat Landrace Selections**

- ◆ **Collected in the 1990's from 10 States in Mexico**
- ◆ **Planted in NW Mexico under drought in 2004 (200 mm available moisture) and heat.**
- ◆ **Two replications, small plots**
- ◆ **Harvested only those with acceptable seed-set**
- ◆ **The best yielded twice as much as best checks from breeders**

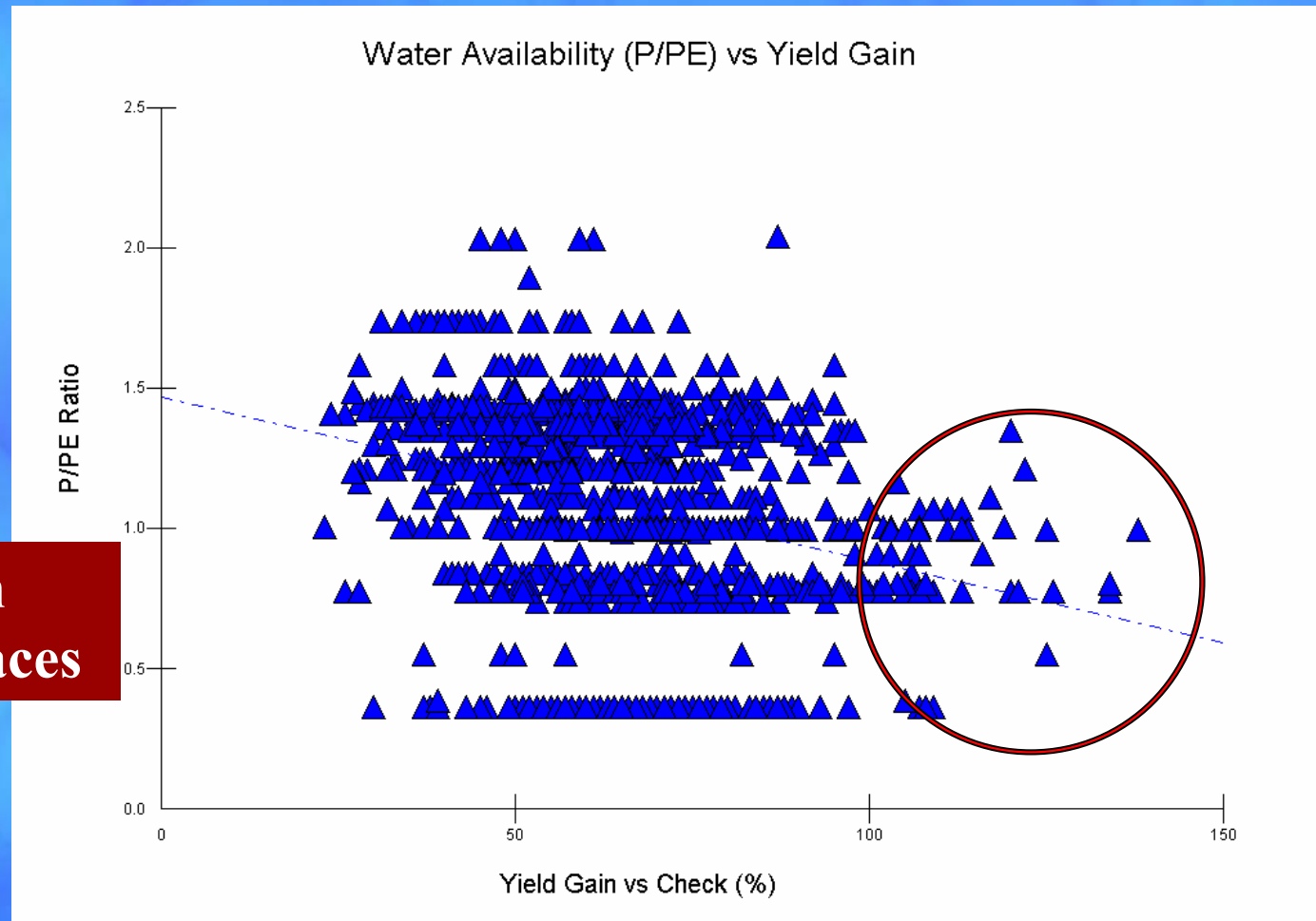


# 10,000 Mexican Wheat Landrace Selections



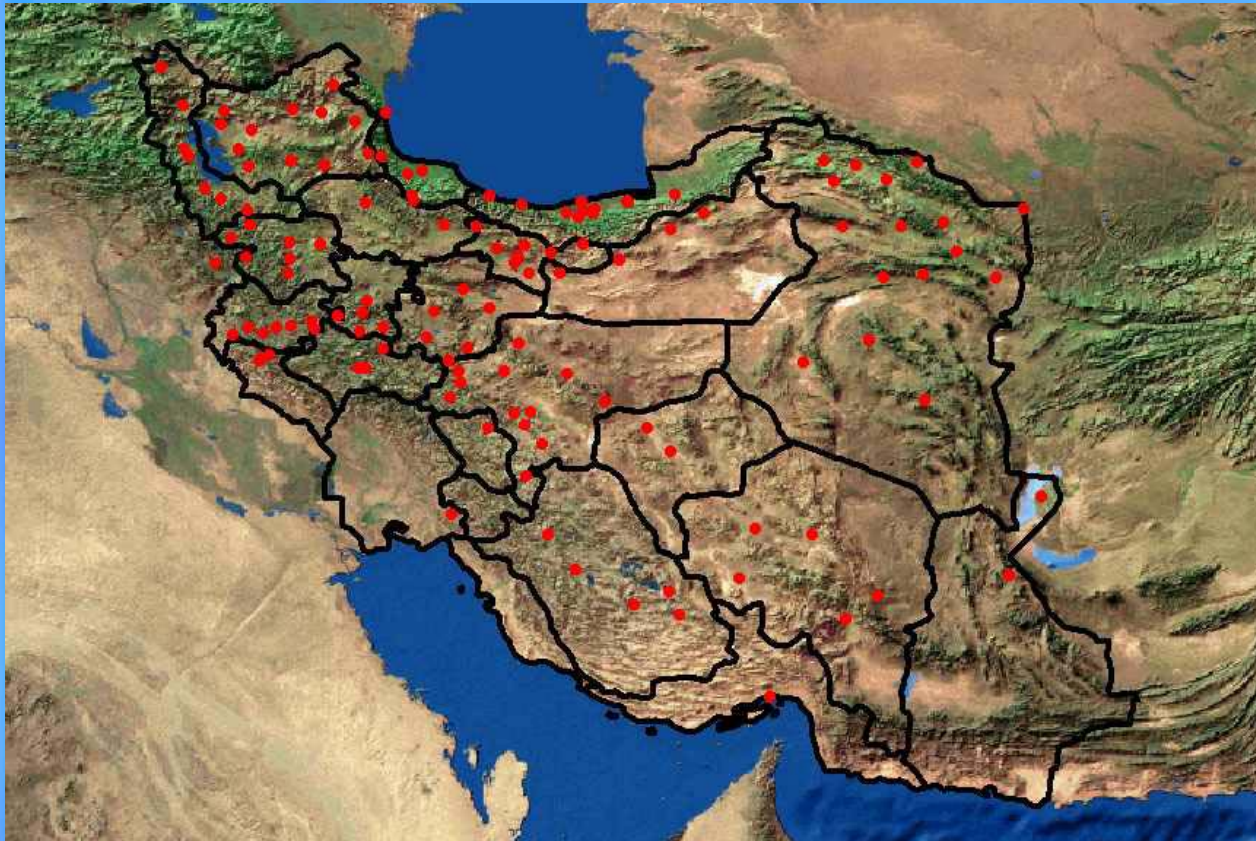
**Drought Tolerance**

# Mexican Wheat Landraces (surviving 1500)



**Diversity between  
and within landraces**

# 10,000 Iranian Wheat Landraces



Waiting in the wings

# Conclusions



- ◆ **GIS will help map area of collection of genebank accessions against background of local edaphic and climatic conditions**
  - ▶ This helps explain:
    - Stress tolerances
    - Adaptation patterns, including those based on TPEs.
- ◆ **GIS will pinpoint regions with present or past wheat production experiencing stresses of interest: e.g. salinity, heat, drought.**
  - ▶ This will allow targeted future collection trips to sample for specific traits:
    - Stress tolerances
    - Quality or micro-nutrient traits

# Conclusions



- ◆ **Results will identify those landrace genotypes most of interest for:**
  - ▶ **In depth study of stress tolerances and adaptation patterns at the level of:**
    - **Physiology**
    - **‘Fine-phenotyping’**
    - **Inheritance**
    - **Gene expression**
    - **Comparative genomics**
    - **Functional genomics**
  - ▶ **Development of molecular marker populations to link novel genes with easily used markers for breeders**



